
WIDEOR (TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.
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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Jan 13 09:28:01 2000; MasPar time 17.23 Seconds
Tabular output not generated. 862.588 Million cell updates/sec

Title: >US-08-978-217-16
Description: (1-371) from US08978217.pep
Perfect Score: 2706
Sequence: 1 MAATCEISNVSNFYFNAMYS.....YKFGKNSGKKEEVEGESRN 371

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r60
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 48.193; Variance 92.105; scale 0.523

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	668	24.7	300	2	ets transcription fac	6.68e-110
2	380	14.0	807	2	ecdysone-induced prot	2.30e-50
3	373	13.8	829	2	ecdysone-induced prot	5.73e-49
4	373	13.8	829	2	ecdysone-induced prot	5.73e-49
5	372	13.7	883	2	ecdysone-induced prot	9.06e-49
6	369	13.6	873	2	ecdysone-induced prot	5.38e-48
7	353	13.0	581	2	ecdysone-induced prot	5.38e-48
8	350	12.9	619	2	ecdysone-induced prot	5.38e-48
9	340	12.6	114	2	ecdysone-induced prot	2.08e-44
10	338	12.5	407	2	ecdysone-induced prot	1.94e-42
11	337	12.5	409	2	ecdysone-induced prot	1.94e-42
12	339	12.5	430	2	ecdysone-induced prot	1.94e-42
13	334	12.3	453	2	ecdysone-induced prot	1.94e-42
14	334	12.3	453	2	ecdysone-induced prot	1.94e-42
15	331	12.2	428	2	ecdysone-induced prot	1.94e-42
16	331	12.2	428	2	ecdysone-induced prot	1.94e-42
17	321	11.9	211	2	ecdysone-induced prot	1.94e-42
18	321	11.9	211	2	ecdysone-induced prot	1.94e-42
19	317	11.7	103	2	ecdysone-induced prot	1.94e-42
20	314	11.6	454	1	ecdysone-induced prot	1.94e-42
21	314	11.6	454	1	ecdysone-induced prot	1.94e-42
22	313	11.6	454	1	ecdysone-induced prot	1.94e-42
23	310	11.5	179	2	ecdysone-induced prot	1.94e-42

24	311	11.5	385	1	S29844	transforming protein	8.85e-37
25	310	11.5	462	1	S35534	adenovirus E1a enhanc	1.38e-36
26	310	11.5	555	1	S24061	transcription factor	1.38e-36
27	305	11.3	173	2	A56646	transcription factor	1.28e-35
28	306	11.3	250	2	A54308	PE-1 protein - human	8.20e-36
29	307	11.3	452	1	S17403	transforming protein	5.26e-36
30	307	11.3	452	1	S17403	transforming protein	5.26e-36
31	305	11.3	486	1	TVHUEG	transforming protein	1.28e-35
32	306	11.3	732	2	S59133	ETS2 repressor factor	8.20e-36
33	306	11.3	732	2	A43315	ETS domain protein ya	8.20e-36
34	306	11.3	761	2	A46193	88K E-26-specific dom	8.20e-36
35	304	11.2	272	2	A54617	transcription factor	2.00e-35
36	304	11.2	453	1	S49013	transcription factor	2.00e-35
37	304	11.2	478	1	S60754	transcription factor	2.00e-35
38	297	11.0	477	1	B46396	transcription factor	4.44e-34
39	297	11.0	477	1	I38893	transcription factor	4.44e-34
40	298	11.0	510	1	S43692	transcription factor	2.85e-34
41	294	10.9	342	2	A46396	ets-related protein 7	1.67e-33
42	273	10.1	472	1	B53236	transcription factor	1.67e-29
43	273	10.1	472	1	A53236	transcription factor	1.67e-29
44	274	10.1	479	1	TYOHE2	transcription factor	1.08e-29
45	271	10.0	268	2	S11224	transcription factor	3.98e-29

ALIGNMENTS

RESULT 1

ENTRY JMW0048 #type complete
TITLE ets transcription factor - mouse
ORGANISM Mus musculus #common_name house mouse
DATE 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999

ACCESSIONS JMW0048
REFERENCE Bocherlt, M.A.; Kleinbaum, L.A.; Sun, L.Y.; Burton, F.H.
#authors Biochem. Biophys. Res. Commun. (1998) 246:176-181
#journal Molecular cloning and expression of Ebf, a new member of the
#title ets transcription factor/oncoprotein gene family.

#cross-references MIM:98262938
#accession JMW0048
##molecule_type mRNA
##residues 1-300 #label BOC
CLASSIFICATION #superfamily ets DNA-binding domain homology
FEATURE #domain ets DNA-binding domain homology #label ETS
209-289 #length 300 #molecular_weight 34903 #checksum 7604

QUERY MATCH
Best Local Similarity 80.8%; Pred. No. 6.68e-110;
Matches 80; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Query Match 24.7%; Score 668; DB 2; Length 300;

Best Local Similarity 80.8%; Pred. No. 6.68e-110;
Matches 80; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Db	201	KHNPGTHLMEFIRDLSPKPNPLIKEDRSEGFELKSEVAOLMGKKNSSMTY	260
Oy	267	KHAPGTHLMEFIRDLSPKPNPLIKEDRSEGFELKSEVAOLMGKKNSSMTY	326
Db	261	EKLSPAMRYKKRELLERVDGRRLVYKFGKNARGNRE	299
Oy	327	EKLSPAMRYKKRELLERVDGRRLVYKFGKNARGNRE	365

RESULT 2

ENTRY A53225 #type complete
TITLE ecdysone-induced protein E74A - fruit fly (Drosophila
ORGANISM Drosophila melanogaster #formal_name Drosophila
DATE 21-Feb-1997 #sequence_revision 12-May-1994 #text_change

ACCESSIONS A53225
REFERENCE Jones, C.W.; Dalton, M.W.; Townley, L.H.
#authors Genetics (1991) 127:535-543
#journal Interspecific comparisons of the structure and regulation of
#title the Drosophila ecdysone-inducible gene E74.

```

#cross-references MUID:91200627
#accession A53225
##status preliminary; not compared with conceptual translation
##molecule_type DNA
##residues 1-807 #label JON
##cross-references GB:X59492
GENETICS
#gene FlyBase:FBse/Elp74EF
##cross-references FlyBase:FBgn0012696
CLASSIFICATION #superfamily ets DNA-binding domain homology
FEATURE
733-793 #domain ets DNA-binding domain homology #label ETS
SUMMARY #length 807 #molecular-weight 85047 #checksum 8801

Query Match 14.0%; Score 380; DB 2; Length 807;
Best Local Similarity 33.1%; Pred. NO. 2,30e-50;
Matches 58; Conservative 51; Mismatches 59; Indels 7; Gaps 7;

Db 623 STIAAAAAAAAAVSSSSAVALAAAMLASAAAAAGSVIOPATSSVSDS-YYLEL 681
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Oy 182 STYCGAPSPGSDSVSTAKTATPOSS-HASDGSDDVDLDTESKVEPRD-DFTDYKGE 239
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 682 GGFQGRKAKRPK-PK-L-E-MGVKRRASREGSTYYLWEFLKLLODDEYCPRFIKWTNR 737
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Oy 240 PKHGRRKRGPRKLSKEYWCDELEKSKSHARGRHWFINDILLIHRBLNGLMKWNRH 299
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 738 KGVFLVDSKAVSRLMGHHKKPKMDNTTNGRALRYIYQRCIGLAKVDGQRLVYQF 792
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Oy 300 EGVFETLRSEAVVAQLMGQKKNSMWTYEKLSRAKRYKKREILERVGRRLVYKF 354

RESULT 3
ENTRY A34692 #type complete
TITLE ecdyso-ne-induced protein E74A - fruit fly (Drosophila melanogaster)
ALTERNATE_NAMES ets-related protein E74A
ORGANISM Drosophila melanogaster
DATE 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Sep-1998

ACCESSIONS
REFERENCE A34692
#authors Burts, K.C.; Thummel, C.S.; Jones, C.W.; Karim, F.D.; Hogness, D.S.
#journal Cell (1990) 61:85-99
#title The Drosophila 74EF early puff contains E74, a complex ecdyso-ne-inducible gene that encodes two ets-related proteins.
#cross-references MUID:90199900
#accession A34692
##molecule_type mRNA
##residues 1-829 #label BUR
##cross-references GB:M37082; NID:91573307; PID:91573308
GENETICS
#gene E74
##cross-references FlyBase:FBgn0000567
CLASSIFICATION #superfamily ets DNA-binding domain homology
KEYWORDS alternative splicing; DNA binding; nucleus; transcription regulation
FEATURE
735-815 #domain ets DNA-binding domain homology #label ETS
SUMMARY #length 829 #molecular-weight 87138 #checksum 9895

Query Match 13.8%; Score 373; DB 2; Length 829;
Best Local Similarity 34.9%; Pred. NO. 5,73e-49;
Matches 59; Conservative 46; Mismatches 57; Indels 7; Gaps 7;

Db 653 SSSSAVAAAAMLSAAAAATAAAAGSGSVIOPATSSV-S-YDIS-YYLELGGFQOR 709
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Oy 186 PGAPSPGSSDVTAKTATPOSSHASDGSDDVDLDTESKVEPRDPTDYKKGPRKGR 245
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 710 KAKPRK-PK-L-E-MGVKRRSREGSTYYLWEFLKLLODDEYCPRFIKWTNRKGVFKL 765
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Oy 246 KRGPRKLSKEYWCDELEKSKSHARGRTHLWEFTRDILLIHRBLNGLMKWNRHGVYKF 305
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

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Db	766	VDSKAVSLTGMHKNRPDMNRTGALRYYYGGIATKGQGLTVYOF	814
Oy	306	LRSFVAQLMGCKKKNSMTYEKLSRPMRYRKREILERPDRGRLLVYKF	354
RESULT	4	B34692 #type complete	
ENTRY		ecdysone-induced protein E74B - fruit fly (<i>Drosophila melanogaster</i>)	
TITLE		ets-related protein E74B	
ALTERNATE_NAMES		#formal_name Drosophila melanogaster	
ORGANISM		07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change	
DATE		24-Sep-1998	
ACCESSIONS		B34692	
REFERENCE		A90912	
#authors		Burtis, K.C.; Thummel, C.S.; Jones, C.W.; Karin, F.D.; Hogness, D.S.	
#journal		Cell (1990) 61:85-99	
#title		The <i>Drosophila</i> 74EF early puff contains E74, a complex ecdysone-inducible gene that encodes two ets-related proteins.	
#cross-references MUID:	90199900		
#accession		B34692	
#molecule_type	DNA		
#residues	1-883	#label BUR	
##cross-references GB:	M37083; NID:g157309; PID:g157310		
GENETICS			
#gene	E74		
.#cross-references FlyBase:	FBgn0000567		
CLASSIFICATION	#superfamily ets DNA-binding domain homology alternative splicing; DNA binding; nucleus; transcription regulation		
KEYWORDS			
FEATURE			
SUMMARY	789-869	#domain ets DNA-binding domain homology #label ETS; #length 883 #molecular_weight 94810 #checksum 2082	
Query Match		13.8%; Score 373; DB 2; Length 883;	
Best Local Similarity	34.9%; Pred. No. 5,73e-49;		
Matches	59; Conservative 46; Mismatches 57; Indels 7; Gaps 7,		
Db	707	SSSSAVALAAAMLSASAAAAATAAAAAGSGSVIQPATSSV-S-YDLS-YMLEIGVFQOR	763
Oy	186	PGAESPSPGSIVSTARTATPQGSASHSDSGSDVDLDTESKVFPDPDDTYKKCGPKHGKR	245
Db	764	KAKPRK-PK-L-E-MGVKRRSRSGSTTYLMFEFLTLQDREVCPRIKKTNRKGYEKL	819
Oy	246	KRGRRKTKSKTYWCLECKSKSHAPRGTHLWFERLDLIHPLELNEGLMKKENRREGVAFK	305
Db	820	VDSKAVSLTGMHKNRPDMNRTGALRYYYGGIATKGQGLTVYOF	868
Oy	306	LRSFVAQLMGCKKKNSMTYEKLSRPMRYRKREILERPDRGRLLVYKF	354
RESULT	5	S04722 #type complete	
ENTRY		puff 74E protein - fruit fly (<i>Drosophila melanogaster</i>)	
TITLE		#formal_name Drosophila melanogaster	
ORGANISM		28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change	
DATE		24-Sep-1998	
ACCESSIONS		S04722	
REFERENCE		Janknecht, R.; Taube, W.; Lueddecke, H.U.; Pongs, O.	
#authors		Nucleic Acids Res. (1989) 17:4455-4464	
#journal		Characterization of a putative transcription factor gene expressed in the 20-OH-ecdysone inducible puff 74EF in <i>Drosophila melanogaster</i> .	
#cross-references MUID:	89315191		
#accession		S04722	
#molecule_type	DNA		
#residues	1-883	#label JAN	
##cross-references EMBL:	X15087; NID:g7513; PID:g7514		
#note		Gln-867 was also found	

```

#gene      FlyBase:Elip74EF
#cross-references FlyBase:Fbgn0000567
CLASSIFICATION #map:position 3 74EF
KEYWORDS #superfamily ets DNA-binding domain homology
FEATURE alternative splicing; DNA binding; transcription regulation
SUMMARY 789-869 #domain ets DNA-binding domain homology #label ETS
          #length 883 #molecular-weight 94819 #checksum 1974

Query Match      13.7%; Score 372; DB 2; Length 883;
Best Local Similarity 34.9%; Pred. No. 9,06e-49;
Matches 59; Conservative 46; Mismatches 57; Indels 7; Gaps 7;

Db 707 SSSSAVAANAAMLSAATAAATAAGSGSVIQTATSV-S-YDLS-YMLELGFGQR 763
      ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Oy 186 PGAPSPGSSDVTARTATPQSSHAASDGSVDLDLTESKVPFPDPTDKKGEPKHGR 245
      ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Oy 246 KAKKPRK-PK-L-E-MGVKRRSREGSTTYLMEFLKLLODREYCPRIKTNREKGYFKL 819
      ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Oy 820 VDSKAVSLTGMHKKRKPDMNMTETGRALRYYYGRIIAKYDGRGLVYHF 868
      ::: ::::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Oy 306 LRSEVAQLDVGOKKKNSMNTYKLSRAMRYTYKREILERVDRGLRYKF 354

RESULT 6
ENTRY B53225 #type complete
TITLE ecdysonine-induced protein E74A - fruit fly (Drosophila virilis)
ORGANISM #format_name Drosophila virilis
DATE 12-May-1994 #sequence_revision 12-May-1994 #text_change 21-Feb-1997
ACCESSIONS B53225
REFERENCE A53225
#authors Jones, C.W.; Dalton, M.W.; Townley, L.H.
#journal Genetics (1991) 127:535-543
#title Interspecific comparisons of the structure and regulation of the
      the Drosophila ecdysonine-inducible gene E74.
#cross-references MUID:91200627
#accession B53225
##status Preliminary: not compared with conceptual translation
##molecule_type mRNA
##residues 1-873 #label JON
##cross-references GB:X59493

#gene FlyBase:Dv4r/Elip74EF
CLASSIFICATION #cross-references FlyBase:Fbgn0013076
FEATURE #superfamily ets DNA-binding domain homology
SUMMARY 779-959 #domain ets DNA-binding domain homology #label ETS
          #length 873 #molecular-weight 94630 #checksum 6269

Query Match      13.6%; Score 369; DB 2; Length 873;
Best Local Similarity 47.3%; Pred. No. 3,58e-48;
Matches 43; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Db 768 KRASRGSTTYLMEFLKLLODREYCPRIKTNREKGYKRLVDSKAVSRKMGHKKRPD 827
      ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Oy 264 KRSKAPRGTLMEFIRILLHPLEINELGMENRHHGVFEFLRSEAVADLMGOKKKNSN 323
      ::: ::::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Oy 828 MNVETMGRLRYRYORGILAKVDORLTYOF 858
      ::: ::::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Oy 324 MTYEKLSRAMRYTYKREILERVDRGLRYKF 354

RESULT 7
ENTRY G02318 #type complete
TITLE Ets transcription factor - human
ORGANISM #format_name Homo sapiens #common_name man
DATE 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998

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ACCESSIONS      G02318
REFERENCE        H01044
#authors         Libermann, T.
#submission      Submitted to the EMBL Data Library, December 1995
#accesion        G02318
#status          Preliminary; translated from GB/EMBL/DDb
#molecule-type  mRNA
#residues        1-581 #label LIB
#cross-references EMBL:U43188; NID:g1420888; PID:g1420889
GENETICS
#gene            NEF-2
CLASSIFICATION   #superfamily ets DNA-binding domain homology
FEATURE
#feature         198-278
SUMMARY          #domain ets DNA-binding domain homology #label ETS
                  #length 581 #molecular-weight 62711 #checksum 2023

Query Match     13.0%; Score 353; DB 2; Length 581;
Best Local Similarity 44.6%; Pred. NO.5.33e-45;
Matches 41; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

Db 186 KKPRGKNTYTLLEFFLDLDQKNCPPRIKWTOREKGIFKLVDSKAVSLKMGKKKP 245
    ||::| |::||::| |::| |::| |::| |::| |::| |::| |::| |::|
Qy 264 KKSRIA-PRGHLMFEFLDILIHEDLEGSLMKENHCEGVFKLRSEANAQLMGCKKKNS 322
    :|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
Qy 323 NMTEKLSRAARYYYKRILEIRVDRGLRYKF 354

RESULT 8
ENTRY    A43361 #type complete
TITLE    Ets-related transcription factor Elf-1 - human
ALTERNATE_NAMES
ORGANISM #formal_name Homo sapiens #common_name man
DATE      11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change
          15-Aug-1997

ACCESSIONS
REFERENCE
#authors      Leiden, J.M.; Wang, C.Y.; Petryniak, B.; Markovitz, D.M.;
              Nabel, G.J.; Thompson, C.B.
#journal      J. Virol. (1992) 66:5890-5897
#citle       A novel Ets-related transcription factor, Elf-1, binds to
              human immunodeficiency virus type 2 regulatory elements
              that are required for inducible trans activation in T
              cells.
#accession    A43361
#molecule-type mRNA
#residues     1-619 #label LEI
#cross-references GB:M62882
REFERENCE
#authors      Thompson, C.B.; Wang, C.Y.; Ho, I.C.; Bohjanen, P.R.;
              Petryniak, B.; June, C.H.; Miesfeldt, S.; Zhang, L.; Nabel,
              G.J.; Karpinski, B.; Leiden, J.M.
#journal      Mol. Cell. Biol. (1992) 12:1043-1053
#citle       cis-acting sequences required for inducible interleukin-2
              enhancer function bind a novel Ets-related protein, Elf-1.
#cross-references MIMD:92186836
#accession    A42122
#status       Preliminary; not compared with conceptual translation
#molecule-type mRNA
#residues     204-282, 'G', 284-289 #label THO
#experimental_source T-cells
#note         sequence extracted from NCBI backbone (NCBIP:88288)
GENETICS
#gene         GDB:ELF1
#cross-references GDB:131648
CLASSIFICATION #map_position 1p36-1p36
                #superfamily ets DNA-binding domain homology
KEYWORDS       DNA binding; transcription regulation
FEATURE
#feature       210-290
SUMMARY        #domain ets DNA-binding domain homology #label ETS
                #length 619 #molecular-weight 67455 #checksum 5026

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[illegible]

